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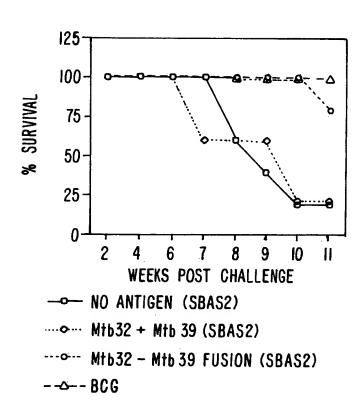
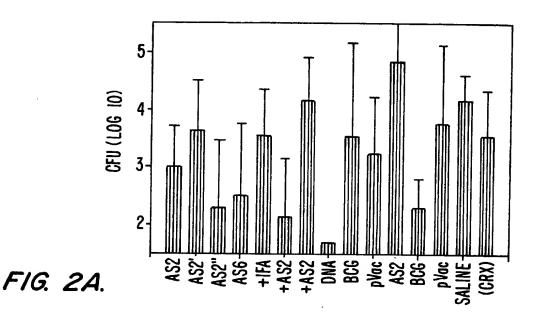
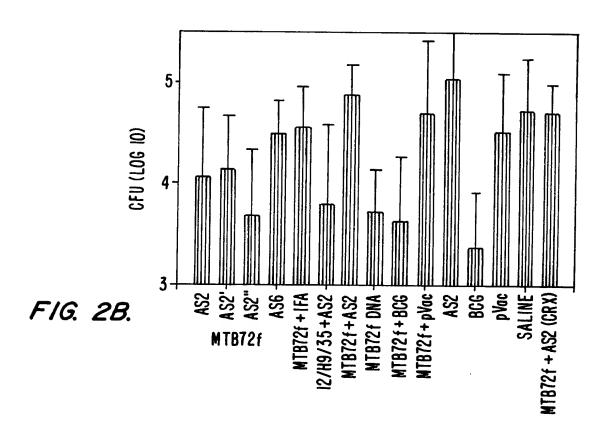


FIG. 1.

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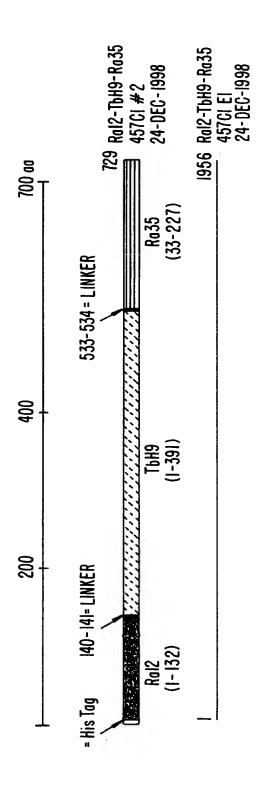
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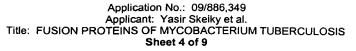




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140 280 350 420 490 560 tgggcgccgg tccgcgatgg cgccaccgac cgcacccagg gcctggcagg gcgtcgcggt ttgaacgggt taggacaggt cctcgacccg aacaacgccg cgggtatgac cgaagagaca tgatcgcggg atcggtggcg cccgtgcggt gtcaacggcc ccgcgctgcc actgggctac ggcggaacgc tgaccggtgc aacaaccacg tcgatgtggt atcggcggcg cgggcccgtc gccgacttcc tcaacaccaa cgtgctgacc acctacggcg tcggattcgc gtggcctacc gtgattcggg cggtgggcag ggaccggttc gtggtcaaca ccaacggtgt atccagcccg ctccggccaa cgcggtgccg tgggcaacag cgtgcaggcg cgtcctag ccttgtcgca tcagcgtcgg ggggccacag gtcatcgatc gctgcagctg gtcgtcgcga tcggccaaac cgatgccgcg aacacggccg gcccgccgg tcgcccaagt gaccggcatc atcaatgcgt atgtcgcggt tggtgagccc gtggtcgcgc tgatccagtt ggtcggtatg

Ra35 N-terminus DNA

sednence acid amino N-terminus 35 Ra,

4/9 Bla Ser Pro Asp Len Pro Len Ala 15 Pro Phe Asp Ala Phe Arg Asp Gln Ser Len S Q Al Pro Pro Ala

Val ά Al Asn Asn Tyr Gly Lys Leu Thr Asn 35 Ile Asn Val Val Gln Pro G1yVal 25

Gln

Ala

Val

Met

Ala Φ Val His Asn Asn Thr 9 Len Gly Val Val Asn 55 ProAsp Ile Val Ile Gly Thr GlyAla Gly

Gly Val Val Asp 85 Gly Val ${
m Tyr}$ Gln Thr Gly Gly Ser Val Ser 75 Phe Ala Asn Ile Asp 70 Thr Ala G1y

Ala Ser Pro Len Gly Gly 1 Gly Ala Arg Gln Leu 100 Len Val Ala Val Asp Gln Thr Arg Asp Tyr

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THE THEMPS

| 31y | Leu | Ser | |
|---|--|--|--|
| 31y (| Se r | Asp : | |
| 31n (130 | Asp | 31y / | |
| 31y (| Ser i | Pro (| Ser 195 |
| 31y (| Ala : 150 | 31n | 41a |
| Ser (| 31n / | []e | 41a <i>i</i> |
| Asn S | Val (| Ala 170 | ľhr i |
| Gly 7 | Thr ' | Ala / | Asn (|
| Met | gln ' | Asp | Met 7 |
| Ala | G1y 145 | Phe | Gly |
| Val | Leu | Gln | Val (|
| Val | Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu 145 | Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser 170 | Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser 185 FIG. 4. (CONTINUED) |
| Pro 120 | Val | Leu | Gln 7G. |
| Glu | Val | $Gl\mathtt{y}$ | Gly 185 |
| G1y | Arg 140 | | Leu |
| Val | Gly | Leu | $Gl\mathtt{y}$ |
| Ala | Pro | Thr 160 | Val Val Asn Gly Leu 180 |
| Val 115 | Val | Glu | Val |
| Gly | Ala | Glu | Val 180 |
| Ile Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly Gly Gly Gly Gly Gly 120 125 | Thr Pro Arg Ala Val Pro Gly Arg 135 | Gly Ala Glu Glu Thr Leu Asn 160 | Gly Gly Pro |
| Gly | Pro | Gly | $G1\mathtt{y}$ |
| Ile | Thr | Thr 155 | $\text{Gl}\gamma$ |



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MHHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLG Mtb72f-mutSA MHHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLG Mtb72f

Ra12

LGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHH Mtb72f 56 56

LGVVDNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHH Mtb72f-mutSA **TDH9FL**

PGDVISVTWQTKSFFTRTFNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSAS Mtb72f-mutSA PGDVISVTWQTKSFFTRTFNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSAS Mtb72f 111 111

LVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSV Mtb72f-mutSA LVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSV Mtb72f 166 166

Mtb72f-mutsA Mtb72f TAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAI TAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAI

AVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVE Mtb72f-mutSA Mtb72f AVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVE 276 276

EASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM Mtb72f-mutSA EASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM Mtb72f 331 331

ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSS Mtb72f-mutSA ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAQAVQTAAQNGVRAMSSLGSSLGSS Mtb72f 386 386

GLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQM Mtb72f-mutSA GLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQM Mtb72f 441 441

FIG. 5

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LGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDJAPPALSQDRFADFPAL Mtb72f-mutSA PLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDI Mtb72f-mutSA Mtb72f PLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNNVIAGATDI Mtb72f 496 LGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDJAPPALSQDRFADFPAL Ra35 496 551 551

NAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN Mtb72f-mutSA NAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN Mtb72f 909 909

SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVV Mtb72f-mutSA SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVV Mtb72f 661 661

716 NGLGQVVGMNTAAS 716 NGLGQVVGMNTAAS

Mtb72f-mutSA

Mtb72f

FIG. 5. (CONTINUED)



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TbRa35 mutSA TbRa35 mat VGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQ VGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQ 51 51

TbRa35 mutSA

TbRa35 mat

MHHHHHHAPPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNA

Ra35 N-term

MHHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNA

DVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVA TbRa35 mutSA DVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVA TbRa35 mat 101 101

Ral2 Cterm

LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNHA TbRa35 mutSA LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNFA TbRa35 mat end Ra35 Nterm 151 151

ASPNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV TbRa35 mutSA ASPNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV TbRa35 mat 201 201

DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH TbRa35 mutSA DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH TbRa35 mat 251 251

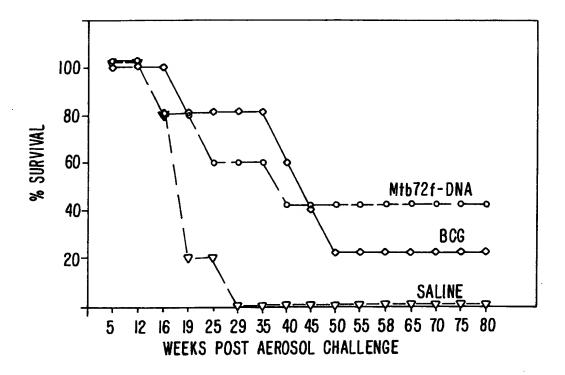
Ra12 end HPGDVISVTWQTKSGGTRTGNVTLAEGPPA HPGDVISVTWQTKSGGTRTGNVTLAEGPPA 301 301

TbRa35 mutSA TbRa35_mat



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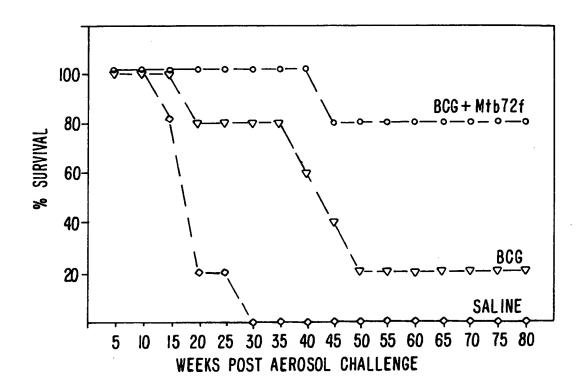


FIG. 7.